

AMENDMENTS TO THE SPECIFICATION:

Please amend the paragraph on page 2, line 34 – page 3, line 2 as follows:

Fig. 4 shows pH-stability curves similar to Fig. 1 but for ~~six~~^{five} other acid-stable proteases of the subtilisin family derived from *Bacillus alcalophilus* NCIMB 10438, *Fusarium oxysporum* IFO 4471, *Paecilomyces lilacinus* CBS 102449, ~~*Aspergillus* sp. CBS 102448~~, *Acremonium chrysogenum* ATCC 48272, *Acremonium kiliense* ATCC 20338;

Please amend the paragraph on page 5, line 34 as follows:

(i) the proteases derived from *Bacillus* sp. NCIMB 40484, *Bacillus alcalophilus* NCIMB 10438; *Fusarium oxysporum* IFO 4471; *Paecilomyces lilacinus* CBS 102449, ~~*Aspergillus* sp. CBS 102448~~, *Acremonium chrysogenum* ATCC 48272, and *Acremonium kiliense* ATCC 20338;

Please amend the table on page 29, lines 2-4 as follows:

Protease / subtilisin from	A_{280}/A_{280}
Sub Novo	2.11
Sub.Novo(Y217L)	2.12
SAVINASE™	2.12
<i>Bacillus</i> sp., NCIMB 40484	2.19
<i>Bacillus alcalophilus</i> , NCIMB 10438	1.92
<i>Fusarium oxysporum</i> , IFO 4471	1.89
<i>Paecilomyces lilacinus</i> , CBS 102449	1.92
<i>Aspergillus</i> sp., CBS 102448	4.96
<i>Acremonium chrysogenum</i> , ATCC 48272	2.04
<i>Acremonium kiliense</i> , ATCC 20338	1.71

Please amend the paragraph on page 36, lines 11-17 as follows:

The proteases of *Fusarium oxysporum* IFO 4471, *Bacillus alcalophilus* NCIMB 10438, *Paecilomyces lilacinus* CBS 102449, ~~*Aspergillus* sp. CBS 102448~~, *Acremonium chrysogenum* ATCC 48272, and *Acremonium kiliense* ATCC 20388 were prepared using conventional methods, as generally described above for the protease of *Bacillus alcalophilus*, NCIMB 10438.

Please amend the paragraph on page 37, lines 29-33 as follows:

The proteases prepared from *Bacillus alcalophilus* NCIMB 10438, *Fusarium oxysporum* IFO 4471, *Paecilomyces lilacinus* CBS 102449, ~~*Aspergillus* sp. CBS 102448~~, *Acremonium chrysogenum* ATCC 48272, *Acremonium kiliense* ATCC 20338 are all subtilisins.

Please amend the table on page 38, lines 1-3 as follows:

Protease	SDS-PAGE Purity (Area %)
<i>Bacillus alcalophilus</i> NCIMB 10438	100.0
<i>Fusarium oxysporum</i> IFO 4471	n.d.
<i>Paecilomyces lilacinus</i> CBS 102449	98.3
<i>Aspergillus</i> sp. CBS 102448	n.d.
<i>Acremonium chrysogenum</i> ATCC 48272	98.6
<i>Acremonium kiliense</i> ATCC 20338	n.d.

n.d. = not determined

Please amend the table on page 38, lines 17-end as follows:

Protease	pH- optimum	Temperature- optimum (°C)
<i>Bacillus alcalophilus</i> NCIMB 10438	9	70
<i>Fusarium oxysporum</i> IFO 4471	11	60
<i>Paecilomyces lilacinus</i> CBS 102449	8	60
<i>Aspergillus</i> sp. CBS 102448	10	60
<i>Acremonium chrysogenum</i> ATCC 48272	9	70
<i>Acremonium kiliense</i> ATCC 20338	11	70

Please amend the table on page 39, lines 1-4 as follows:

Protease \ pH	2.0	2.5	3.0	3.5	4.0	4.5	5.0
Bacillus alcalophilus NCIMB 10438	0.007	0.005	0.175	0.844	0.965	1.017	1.038
Fusarium oxysporum IFO 4471	0.000	0.000	0.003	0.649	0.929	1.030	1.056
Paecilomyces lilacinus CBS 102449	0.002	0.003	0.005	0.450	0.897	1.000	0.947
Aspergillus sp. CBS 102448	0.002	0.002	0.002	0.532	0.860	0.970	0.976
Acremonium chrysogenum ATCC 48272	0.002	0.001	0.001	0.809	0.894	0.972	1.005
Acremonium kiliense ATCC 20338	0.008	0.003	0.023	0.412	0.843	0.955	1.009

Please amend the table on the bottom of page 40 as follows:

Protease, subtilisin from	Residual activity (%)
Bacillus sp., NCIMB 40484	4.3
Bacillus amyloliquefaciens	0.1
Bacillus amyloliquefaciens (Y217L)	0.0
Bacillus clausii, (Savinase®)	0.0
Bacillus alcalophilus, NCIMB 10438	0.0
Fusarium oxysporum IFO 4471	0.1
Paecilomyces lilacinus, CBS 102449	0.1
Aspergillus sp., CBS 102448	0.1
Acremonium chrysogenum, ATCC 48272	0.1
Acremonium kiliense, ATCC 20338	n.d.*

Please amend the table on page 41, lines 13-14 as follows:

Protease, subtilisin from	FITC /(+/ -20000)
Bacillus alcalophilus NCIMB 10438	81300
Fusarium oxysporum IFO 4471	102200
Paecilomyces lilacinus CBS 102449	98700
Aspergillus sp. CBS 102448	123400
Acremonium chrysogenum ATCC 48272	89600
Acremonium kiliense ATCC 20338	94600
Protease I	-9200
Protease II	-1200